MICROBES, RESISTANCE, AND LIFESTYLE: A METAGENOMIC SURVEY TO REVEAL CARRYING ANTIMICROBIAL RESISTANCES IN ANCESTRAL HUMAN COMMUNITIES

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RESUMEN

The study of antimicrobial resistance (AMR) is one of the hot topics in clinical microbiology and infection. The widespread AMRs is conceptually linked to antimicrobial drug abuse based on increasing its therapeutic misuse and uncontrolled distribution, in addition to failed policies for residue treatment to avoid environmental pollution with such synthetic compounds. Consequently, antibiotic exposure and concomitant AMRs are closely linked to industrialised and developing societies, where access to clinical monitoring often reveals multidrug-resistant strains and underlying genetic elements that confer such traits. However, ancestral communities are predominantly neglected in such a survey, making it impossible to assess whether they are naturally exposed or are a reservoir of AMRs. By conducting a comprehensive assessment of traditional and westernised populations from various countries using a multi-continent approach, we have identified signatures of AMRs in populations with different levels of isolation from urban settlements. Despite their apparent lack of contact with urban societies, we uncovered a particular resistome gradient across various populations, suggesting the true degree of isolation and contact with closer industrialised settlements. Moreover, we identified the Brazilian Yanomami and the Tanzanian Hadza as a near clusters based on taxonomy and AMR compositions, despite their distant geographical localisations. This fact suggests a specific gut microbial signature of a traditional lifestyle with potential ancestral AMR composition.

Palabras claves: *antimicrobial resistance, intestinal microbiome, traditional populations, lifestyle, Yanomami.*